

IFWO

RAW SEQUENCE LISTING

DATE: 08/04/2004 TIME: 08:22:56

PATENT APPLICATION: US/10/663,158

Input Set : A:\Sequence Listing.txt Output Set: N:\CRF4\08042004\J663158.raw

3 <110> APPLICANT: Desauvage, Frederic Grewal, Iqbal Gurney, Austin L. 7 <120> TITLE OF INVENTION: TYPE I CYTOKINE RECEPTOR TCCR 9 <130> FILE REFERENCE: 11669.123USC1 11 <140> CURRENT APPLICATION NUMBER: US 10/663,158 12 <141> CURRENT FILING DATE: 2003-09-15 14 <150> PRIOR APPLICATION NUMBER: US 09/692,504 15 <151> PRIOR FILING DATE: 2000-10-18 17 <150> PRIOR APPLICATION NUMBER: US 60/160,542 18 <151> PRIOR FILING DATE: 1999-10-20 20 <160> NUMBER OF SEQ ID NOS: 16 22 <170> SOFTWARE: PatentIn version 3.1 24 <210> SEQ ID NO: 1 25 <211> LENGTH: 636 26 <212> TYPE: PRT 27 <213> ORGANISM: Homo sapiens 29 <400> SEQUENCE: 1 31 Met Arg Gly Gly Arg Gly Ala Pro Phe Trp Leu Trp Pro Leu Pro Lys 35 Leu Ala Leu Leu Pro Leu Leu Trp Val Leu Phe Gln Arg Thr Arg Pro 39 Gln Gly Ser Ala Gly Pro Leu Gln Cys Tyr Gly Val Gly Pro Leu Gly 43 Asp Leu Asn Cys Ser Trp Glu Pro Leu Gly Asp Leu Gly Ala Pro Ser 47 Glu Leu His Leu Gln Ser Gln Lys Tyr Arg Ser Asn Lys Thr Gln Thr 70 51 Val Ala Val Ala Ala Gly Arg Ser Trp Val Ala Ile Pro Arg Glu Gln 90 55 Leu Thr Met Ser Asp Lys Leu Leu Val Trp Gly Thr Lys Ala Gly Gln 100 105 59 Pro Leu Trp Pro Pro Val Phe Val Asn Leu Glu Thr Gln Met Lys Pro 120 63 Asn Ala Pro Arg Leu Gly Pro Asp Val Asp Phe Ser Glu Asp Asp Pro 67 Leu Glu Ala Thr Val His Trp Ala Pro Pro Thr Trp Pro Ser His Lys 150 155 71 Val Leu Ile Cys Gln Phe His Tyr Arg Arg Cys Gln Glu Ala Ala Trp 165 170 75 Thr Leu Leu Glu Pro Glu Leu Lys Thr Ile Pro Leu Thr Pro Val Glu 180

185

79 Ile Gln Asp Leu Glu Leu Ala Thr Gly Tyr Lys Val Tyr Gly Arq Cys

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80	195			200					205			
83 Arg Met		Glu Gl	u Asp		Trp	Gly	Glu	Trp		Pro	Ile	Leu
84 210	•		215		-	•		220				
87 Ser Phe	Gln Thr	Pro Pr	o Ser	Ala	Pro	Lys	Asp	Val	Trp	Val	Ser	Gly
88 225		23					235					240
91 Asn Leu	Cys Gly	Thr Pi	o Gly	Gly	Glu	Glu	Pro	Leu	Leu	Leu	Trp	Lys
92		245				250					255	
95 Ala Pro		Cys Va	al Gln	Val		Tyr	Lys	Val	Trp		Trp	Val
96	260		_	~7	265			~	_	270	_	_
99 Gly Gly		Leu Se	er Pro			шe	Thr	Cys	_	_	Ser	Leu
100 103 Ile Pro	275	, 71 n (ירי ירי	280 - זוג		. 17-1	Cor	~ 7\ T ~	285		, 7\ T ~	. The
103 TTE PTO	Ser Gry	y Ala C	29!	-	a Arg	vai	ser	300		. ASI	LAIC	1111
107 Ser Trp	Glu Pro	o Leu 1			ı Ser	Len	Val			Asr	Ser	· Ala
108 305	OIG II		310	. дес		псс	315	_	ДСС		, DCI	320
111 Ser Ala	Pro Arc			a Val	Ser	Ser			Gly	ser Ser	Thr	
112	•	325				330			-		335	
115 Leu Leu	Val Thi	r Trp (ln Pro	o Gly	/ Pro	Gly	Glu	Pro	Let	ı Glu	His	. Val
116	340)			345					350)	
119 Val Asp	Trp Ala	a Arg A	sp Gly	y Asr	Pro	Leu	Glu	ı Lys	Let	ı Asn	Trp	Val
120	355			360					365			
123 Arg Leu	1	o Gly A			Ala	Leu	Leu			Asn	Phe	Thr
124 370			379		7			380			~	~7
127 Val Gly	val Pro			e Tnr	. vai	Thr			ser	: Ala	Ser	_
128 385 131 Leu Ala	Ser Ala		190 Ser Va	l Trr	. Clu	Dho	395		Gla	ι Τ.σ.:	בות	400
132 Lea A1a	DCI AIC	405	ci va.		, Gra	410	_	GIU	GIU	т пес	415	
135 Leu Val	Glv Pro		eu Tro) Arc	ı Leu			Ala	Pro	Pro		
136	420				425					430	_	
139 Pro Ala	Ile Ala	a Trp (ly Glu	ı Val	Pro	Arg	His	Gln	Lev	Arg	Gly	His
140	435			440					445	_	_	
143 Leu Thr	His Tyr	Thr I	eu Cys	a Ala	Gln	Ser	Gly	Thr	Ser	Pro	Ser	Val
144 450		٠	455					4 60				
147 Cys Met	Asn Val		_	1 Thr	Gln	Ser			Leu	Pro	Asp	
148 465	~~ ~		70	_		_,	475		1		_ ~	480
151 Pro Trp	GIY Pro		Lu Leu	ı Trp) Val			Ser	Thr	· lle		
152 155 Gln Gly	Dro Dro	485	oro Tla	. T.O.	7.00	490		. T.O.	Dro	, 7 an	495	
155 GIII GIY	500		10 116	: пес	505		пте	, пеи	PIC	, Asp 510		LIIIL
159 Leu Arg			en Pro	o Gla			Phe	Len	Trr			Phe
160	515			520		200			525			
163 Leu Leu		Gly I	eu Sei			Thr	Ser	Gly			Tyr	His
164 530		-	535					540	_	-	•	
167 Leu Arg	His Lys	Val I	eu Pro	Arg	Trp	Val	Trp	Glu	Lys	Val	Pro	Asp
168 545		5	50				555	,				560
171 Pro Ala	Asn Ser		er Gly	, Gln	Pro	His	Met	Glu	Gln	Val	Pro	Glu
172		565	•		_	570					575	
175 Ala Gln		_	sp Lei	ı Pro			Glu	Val	Glu			Glu
176	580)			585					590		

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179 Pro Pro Pro Val Met Glu Ser Ser Gln Pro Ala Gln Ala Thr Ala Pro 595 600 183 Leu Asp Ser Gly Tyr Glu Lys His Phe Leu Pro Thr Pro Glu Glu Leu 615 187 Gly Leu Leu Gly Pro Pro Arg Pro Gln Val Leu Ala 188 625 630 191 <210> SEQ ID NO: 2 192 <211> LENGTH: 623 193 <212> TYPE: PRT 194 <213> ORGANISM: Mus musculus 196 <400> SEQUENCE: 2 198 Met Asn Arg Leu Arg Val Ala Arg Leu Thr Pro Leu Glu Leu Leu Leu 199 1 202 Ser Leu Met Ser Leu Leu Gly Thr Arg Pro His Gly Ser Pro Gly 206 Pro Leu Gln Cys Tyr Ser Val Gly Pro Leu Gly Ile Leu Asn Cys Ser 210 Trp Glu Pro Leu Gly Asp Leu Glu Thr Pro Pro Val Leu Tyr His Gln 55 214 Ser Gln Lys Tyr His Pro Asn Arg Val Trp Glu Val Lys Val Pro Ser 215 65 70 218 Lys Gln Ser Trp Val Thr Ile Pro Arg Glu Gln Phe Thr Met Ala Asp 85 90 222 Lys Leu Leu Ile Trp Gly Thr Gln Lys Gly Arg Pro Leu Trp Ser Ser 100 105 226 Val Ser Val Asn Leu Glu Thr Gln Met Lys Pro Asp Thr Pro Gln Ile 120 230 Phe Ser Gln Val Asp Ile Ser Glu Glu Ala Thr Leu Glu Ala Thr Val 130 135 234 Gln Trp Ala Pro Pro Val Trp Pro Pro Gln Lys Ala Leu Thr Cys Gln 150 238 Phe Arg Tyr Lys Glu Cys Gln Ala Glu Ala Trp Thr Arg Leu Glu Pro 165 170 242 Gln Leu Lys Thr Asp Gly Leu Thr Pro Val Glu Met Gln Asn Leu Glu 180 185 246 Pro Gly Thr Cys Tyr Gln Val Ser Gly Arg Cys Gln Val Glu Asn Gly 195 200 205 250 Tyr Pro Trp Gly Glu Trp Ser Ser Pro Leu Ser Phe Gln Thr Pro Phe 210 215 254 Leu Asp Pro Glu Asp Val Trp Val Ser Gly Thr Val Cys Glu Thr Ser 230 235 258 Gly Lys Arg Ala Ala Leu Leu Val Trp Lys Asp Pro Arg Pro Cys Val 245 250 262 Gln Val Thr Tyr Thr Val Trp Phe Gly Ala Gly Asp Ile Thr Thr Thr 260 265 266 Gln Glu Glu Val Pro Cys Cys Lys Ser Pro Val Pro Ala Trp Met Glu 280 270 Trp Ala Val Val Ser Pro Gly Asn Ser Thr Ser Trp Val Pro Pro Thr 295 300

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```
274 Asn Leu Ser Leu Val Cys Leu Ala Pro Glu Ser Ala Pro Cys Asp Val
275 305
                       310
                                           315
278 Gly Val Ser Ser Ala Asp Gly Ser Pro Gly Ile Lys Val Thr Trp Lys
                                       330
282 Gln Gly Thr Arg Lys Pro Leu Glu Tyr Val Val Asp Trp Ala Gln Asp
               340
                                   345
286 Gly Asp Ser Leu Asp Lys Leu Asn Trp Thr Arg Leu Pro Pro Gly Asn
                               360
290 Leu Ser Thr Leu Leu Pro Gly Glu Phe Lys Gly Gly Val Pro Tyr Arg
    370
                           375
                                               380
294 Ile Thr Val Thr Ala Val Tyr Ser Gly Gly Leu Ala Ala Pro Ser
                       390
                                           395
298 Val Trp Gly Phe Arg Glu Glu Leu Val Pro Leu Ala Gly Pro Ala Val
                   405
                                       410
302 Trp Arg Leu Pro Asp Asp Pro Pro Gly Thr Pro Val Val Ala Trp Gly
                                   425
                                                       430
306 Glu Val Pro Arg His Gln Leu Arg Gly Gln Ala Thr His Tyr Thr Phe
           435
                               440
310 Cys Ile Gln Ser Arg Gly Leu Ser Thr Val Cys Arg Asn Val Ser Ser
                           455
314 Gln Thr Gln Thr Ala Thr Leu Pro Asn Leu His Ser Gly Ser Phe Lys
                       470
                                           475
318 Leu Trp Val Thr Val Ser Thr Val Ala Gly Gln Gly Pro Pro Gly Pro
                   485
                                       490
322 Asp Leu Ser Leu His Leu Pro Asp Asn Arg Ile Arg Trp Lys Ala Leu
               500
                                   505
326 Pro Trp Phe Leu Ser Leu Trp Gly Leu Leu Met Gly Cys Gly Leu
327 . 515
                               520
330 Ser Leu Ala Ser Thr Arg Cys Leu Gln Ala Arg Cys Leu His Trp Arg
                           535
334 His Lys Leu Leu Pro Gln Trp Ile Trp Glu Arg Val Pro Asp Pro Ala
338 Asn Ser Asn Ser Gly Gln Pro Tyr Ile Lys Glu Val Ser Leu Pro Gln
                   565
                                       570
342 Pro Pro Lys Asp Gly Pro Ile Leu Glu Val Glu Val Glu Leu Gln
             580
                                   585
346 Pro Val Val Glu Ser Pro Lys Ala Ser Ala Pro Ile Tyr Ser Gly Tyr
347 595
                              600
350 Glu Lys His Phe Leu Pro Thr Pro Glu Glu Leu Gly Leu Leu Val
351 610
                           615
354 <210> SEQ ID NO: 3
355 <211> LENGTH: 2646
356 <212> TYPE: DNA
357 <213> ORGANISM: Homo sapiens
359 <220> FEATURE:
360 <221> NAME/KEY: misc feature
361 <222> LOCATION: (2433)..(2433)
362 <223> OTHER INFORMATION: n is a, c, t, or q
365 <400> SEQUENCE: 3
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```
366 gtgggttegg ettecegttg egeetegggg getgtaceca gagetegaag aggageageg
                                                                              60
     368 eggeeçgeae eeggeaagge tgggeeggae teggggetee egagggaege catgegggga
                                                                             120
     370 ggcaggggeg ececttictg gctgtggeeg etgeccaage tggcgetget geetetqttq
                                                                             180
     372 tgggtgcttt tccagcggac gcgtccccag ggcagcgccg ggccactgca qtqctacqqa
                                                                             240
     374 gttggaccct tgggcgactt gaactgctcg tgggagcctc ttggggacct qqqaqccccc
                                                                             300
     376 teegagttac acetecagag ccaaaagtac egttecaaca aaacecagae tqtqqcaqtq
                                                                             360
     378 gcagccggac ggagctgggt ggccattect cgggaacagc tcaccatgtc tgacaaactc
                                                                             420
     380 cttqtctqqq qcactaaqqc aqqccaqcct ctctqqcccc ccqtcttcqt qaacctaqaa
                                                                             480
     382 acceaaatqa aqceaaacqc ccccqqctq qqccctqacq tqqacttttc cqaqqatqac
                                                                             540
     384 cccctggagg ccactgtcca ttgggcccca cctacatggc catctcataa aqttctgatc
                                                                             600
     386 tgccagttcc actaccgaag atgtcaggag gcggcctgga ccctgctgga accgqagctg
                                                                             660
     388 aagaccatac ccctqacccc tqttqaqatc caaqatttqq aqctaqccac tqqctacaaa
                                                                             720
     390 qtqtatqqcc qctqccqqat qqaqaaaqaa qaqqatttqt qqqqcqaqtq qaqccccatt
                                                                             780
     392 ttgteettee agacacegee ttetgeteea aaagatgtgt gggtateagg gaacetetgt
                                                                             840
     394 gggaegeetg gaggagagga acetttgett etatggaagg ceecagggee etgtgtgeag
                                                                             900
     396 gtgagctaca aagtctggtt ctgggttgga ggtcgtgagc tgagtccaga aggaattacc
                                                                             960
     398 tgctgctgct ccctaattcc cagtggggcg gagtgggcca gggtgtccgc tgtcaacgcc
                                                                            1020
     400 acaagetggg ageeteteae caacetetet ttggtetget tggatteage etetgeeece
                                                                            1080
     402 cgtagcgtgg cagtcagcag catcgctggg agcacggagc tactggtgac ctggcaaccg
                                                                            1140
     404 gggcctgggg aaccactgga gcatgtagtg gactgggctc gagatgggga ccccctggag
                                                                            1200
     406 aaactcaact gggtcegget teeecetggg aaceteagtg etetqttace aqqqaattte
                                                                            1260
     408 actgtcgggg tcccctatcg aatcactgtg accgcagtct ctgcttcagg cttggcctct
                                                                            1320
     410 gcatectecg tetgggggtt cagggaggaa ttagcacccc tagtggggcc aacqetttgg
                                                                            1380
     412 cgactccaag atgcccctcc agggaccccc gccatagcgt ggggagaggt cccaaggcac
                                                                            1440
     414 cagettegag gecaecteae ceactacaee ttgtgtgeae agagtggaae cageceetee
                                                                            1500
     416 gtctgcatga atgtgagtgg caacacacag agtgtcaccc tgcctgacct tccttggggt
                                                                            1560
     418 ccctgtgagc tgtgggtgac agcatctacc atcgctggac agggccctcc tggtcccatc
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     420 ctccggcttc atctaccaga taacaccctg aggtggaaag ttctgccggg catcctattc
                                                                            1680
     422 ttgtgggget tgtteetgtt ggggtgtgge etgageetgg ceaectetgg aaggtgetae
     424 cacctaagge acaaagtget geeegetgg gtetgggaga aagtteetga teetgeeaac
                                                                            1800
     426 agcagttcag gccagcccca catggagcaa gtacctgagg cccagcccct tggggacttg
                                                                            1860
     428 cccatcctgg aagtggagga gatggagccc ccgccggtta tggagtcctc ccagcccgcc
                                                                            1920
     430 caggecaceg ceeegettga etetgggtat gagaageaet teetgeeeac acetgaggag
                                                                            1980
     432 ctgggccttc tggggccccc caggccacag gttctggcct gaaccacacg tctggctggg
                                                                            2040
     434 ggctgccage caggctagag ggatgctcat gcaggttgca ccccagtcct ggattagccc
                                                                            2100
     436 tettgatgga tgaagacaet gaggaeteag agaggetgag teaettaeet gaggaeaece
                                                                            2160
     438 agccaggcag agctgggatt gaaggacccc tatagagaag ggcttggccc ccatggggaa
                                                                            2220
     440 gacacqgatq gaaqqtqqaq caaaqqaaaa tacatqaaat tqaqaqtqqc aqctqcctqc
                                                                            2280
     442 caaaatetgt teegetgtaa cagaactgaa tttggacccc agcacagtgg etcacgeetg
                                                                            2340
     444 taatcccagc actttggcag gccaaggtgg aaggatcact tagagctagg agtttgagac
                                                                            2400
W--> 446 cagcctgggc aatatagcaa qaccctcac tanaaaaata aaacatcaaa aacaaaaaca
                                                                            2460
     448 attagctggg catgatggca cacacctgta gtccgagcca cttgggaggc tgaggtggga
                                                                            2520
     450 ggateggttg ageceaggag ttegaagetg cagggaeete tgattgeace aetgeaetee
                                                                            2580
     2640
     454 aaaaaa
                                                                            2646
     457 <210> SEO ID NO: 4
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458 <211> LENGTH: 2005 459 <212> TYPE: DNA

460 <213> ORGANISM: Mus musculus

RAW SEQUENCE LISTING ERROR SUMMARY PATENT APPLICATION: US/10/663,158

DATE: 08/04/2004 TIME: 08:22:57

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220>

to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 2433

VERIFICATION SUMMARY

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L:446 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:2400